



GeneStream align Home Page

align Search Help

align Results

Please site: *Pearson, W.R., Wood, T., Zhang, Z., and Miller, W. (1997)
Comparison of DNA sequences with protein sequences, Genomics 46: 24-36*

```
>_                                     390 aa vs.
>_                                     76 aa
scoring matrix: , gap penalties: -12/-2
7.4% identity;           Global alignment score: -560

          10          20          30          40          50          60
935757 MAVSESQLKKMVSKYKYRDLTVRETNVNITLYKDLKPVLD SYVFNDGSSRELMNLTGTIP
: .
- MQI-----

          70          80          90          100         110         120
935757 VPYRGNTYNIPICLWLLDTYPYNPPICFVKPTSSMTIKTGKHVDANGKIYLPYLHEWKHP
          : : :          : : :
- -----FVKTL-----TGKTI-----
          10

          130         140         150         160         170         180
935757 QSDLLGLIQVMIVVFGDEPPVFSRPISASYPPYQATGPPNTSYMPGMPGGISPYPGYP
- -----

          190         200         210         220         230         240
935757 NPSGYPGCPYPPGGYPATTSSQYPSQPPVTTVGPSRDGTISED TIRASLISAVSDKLRW
          . : : :          : : :
- -----TLEVEPS-----DTI-----
          20

          250         260         270         280         290         300
935757 RMKEEMDRAQAELNALKRTEEDLKKGHQKLEEMVTRLDQAEVDKNIELLKKKDEELSS
          : : :          : : : :
- -----ENVKA-----KIQDKEG-----
          30

          310         320         330         340         350         360
935757 ALEKMENQSENNDIDEV I IPTAPLYKQILNLYAEENAIEDTIFYLGEALRRGVIDL DVFL
          : : : : :          . : : : :
- -----IP--PDQQR LI-----FAGKQLEDG-----
          40          50
```



370 380 390
935757 KHVRLLSRKQFQLRALMQKARKTAGLSDLY
: : : :
---RTLSDYNIQKESTLHLVLRRLRG---G
60 70

Elapsed time: 0:00:00